

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: November 6, 2004, 19:35:16 ; Search time 12,1875 seconds
(without alignments)
39.474 Million cell updates/sec

Title: US-10-618-644-1
Perfect score: 26
Sequence: 1 YVVF 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databases : PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	132	2 G84717	actin depolymerizing factor 6 [imported] - Arabidopsis thaliana
2	26	100.0	137	2 T43245	probable actin-depolymerizing factor - fission yeast (Schizosaccharomyces pombe)
3	26	100.0	186	2 PQ0200	glycinin G5 - soy
4	26	100.0	191	2 PQ0810	glycinin A3B4 (pla
5	26	100.0	236	2 PQ0806	glycinin A3B4 - so
6	26	100.0	238	2 PQ0809	glycinin A3B4 (pla
7	26	100.0	243	2 PQ0807	glycinin A3B4 - so
8	26	100.0	251	1 S04172	UDP-sugar hydrolas
9	26	100.0	251	2 PQ0808	glycinin A3B4 (pla
10	26	100.0	317	2 E84434	probable phloem-sp
11	26	100.0	338	2 S04331	legumin B (clone p
12	26	100.0	340	2 T24143	hypothetical prote
13	26	100.0	350	2 S00337	legumin B LegK pre
14	26	100.0	373	2 T28978	hypothetical prote
15	26	100.0	449	2 AC0234	probable exported
16	26	100.0	449	2 T47039	hypothetical prote
17	26	100.0	452	2 G86170	hypothetical prote
18	26	100.0	485	2 S44268	legumin B precursor
19	26	100.0	500	2 S26688	legumin K - garden
20	26	100.0	503	2 S00336	legumin B LegJ pre
21	26	100.0	516	1 FWSY3	glycinin G5 precu
22	26	100.0	564	2 S37241	legumin B - fava b
23	26	100.0	566	2 T06453	probable legumin B
24	26	100.0	585	1 EBSAM1	mecl1 protein - St
25	26	100.0	585	2 T44117	methicillin resist
26	26	100.0	585	2 T19692	mecl1 protein - St
27	26	100.0	915	2 T19692	hypothetical prote
28	26	100.0	974	2 S15038	cell division cont
29	26	100.0	1289	2 T31344	GP80 precursor - s

30	26	100.0	3076	2 A87058	fatty acid synthas
31	25	96.2	83	2 T18122	hypothetical prote
32	25	96.2	98	2 T17717	hypothetical prote
33	25	96.2	128	2 H70429	conserved hypotet
34	25	96.2	132	2 B84543	actin depolymerizi
35	25	96.2	158	2 T17748	hypothetical prote
36	25	96.2	161	2 B64106	small protein smps
37	25	96.2	176	2 A71009	hypothetical prote
38	25	96.2	194	2 F64860	hypothetical prote
39	25	96.2	251	2 AF0942	CDPdiacylglycerol
40	25	96.2	258	2 T41936	hypothetical prote
41	25	96.2	265	2 G84434	probable phloem-sp
42	25	96.2	268	2 PQ0199	glycinin A5A4B3 pr
43	25	96.2	270	2 F72259	hypothetical prote
44	25	96.2	272	2 G84435	probable phloem-sp
45	25	96.2	281	2 T05522	hypothetical prote

ALIGNMENTS

RESULT 1

G84717

actin depolymerizing factor 6 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: G84717

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

us, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20081487; PMID:10617197

A:Accession: G84717

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <STO>

A:Cross-references: GB:AE002093; NID:g4432815; PIDN:AAD20665.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g31200

A:Map position: 2

C:Superfamily: cofilin

Query Match 100.0%; Score 26; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVF 5

|||

Db 22 YVVF 26

RESULT 2

T43245

probable actin-depolymerizing factor - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43245; T38120

R:kawamukai, M.

submitted to the EMBL Data Library, December 1996

A:Description: S. pombe cDNA for actin depolymerizing factor.

A:Reference number: Z22362

A:Accession: T43245

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-137 <KAW>

A:Cross-references: UNIPROT:P78929; EMBL:D89939; PIDN:BAAL4039.1

R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z21771

A:Accession: T38120

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A;Residues: 1-137 <CON>
A;Cross-references: EMBL:Z98600; PIDN:CAB11258.1; GSPDB:GN000066; SPDB:SPAC20G4.06c
A;Experimental source: strain 972h-; cosmid c20G4
C;Genetics:
A;Gene: SPAC20G4.06c
A;Map position: 1
A;Introns: 1/3; 37/1
A;Note: adf1
C;Superfamily: cofilin
C;Keywords: actin binding

Query Match 100.0%; Score 26; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVWFK 5
|
|
|
|
Db 27 YVWFK 31

RESULT 3
PQ0200
glycinin Gy5 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: PQ0200
R;Scallan, B.; Thanh, V.H.; Floener, L.A.; Nielsen, N.C.
Theor. Appl. Genet. 70, 510-519, 1991
A;Title: Identification and characterization of DNA clones encoding group-II glycinin subunit
A;Reference number: PQ0199
A;Accession: PQ0200
A;Molecule type: DNA
A;Residues: 1-186 <SCA>
A;Cross-references: UNIPROT:P93708
A;Experimental source: embryo, strain CX635-1-1-1
A;Note: the authors translated the codon NAA for residue 93 as Gln and AGA for residue 94
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;16-186/Product: glycinin B4 chain (fragment) #status predicted <MAT>

Query Match 100.0%; Score 26; DB 2; Length 186;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YVWFK 5
|
|
|
|
Db 136 YVWFK 140

RESULT 4
PQ0810
Glycinin A3B4 (plaamid PSPGD41) - Glycine soja (strain L582) (fragment)
N;Alternate names: 11S globulin; basic and acidic chains
N;Contains: glycinin B4 chain
C;Species: Glycine soja
C;Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: PQ0810
R;Zakharova, E.S.; Epishin, S.M.; Vinetski, Y.P.
Theor. Appl. Genet. 78, 852-856, 1989
A;Title: An attempt to elucidate the origin of cultivated soybean via comparison of nucleotide sequences of the genes for the 11S globulin and the 7S globulin
C;Superfamily: glycinin
C;Keywords: seed; storage protein
F;39-191/Product: glycinin B4 chain #status predicted <GB4>

Query Match 100.0%; Score 26; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A;Reference number: Z19844
 A;Accession: T24143
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-340 <WIL>
 A;Cross-references: UNIPROT:O17998; EMBL:Z81576; PIDN:CAB04643.1; GSPDB:GN00023; CESP:R10E8
 A;Experimental source: clone R10E8
 C;Genetics:
 A;Gene: CESP:R10E8.1
 A;Map position: 5
 A;Introns: 13/2; 34/2; 253/3; 331/3

Query Match 100.0%; Score 26; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVF 5
 |||||
 Db 67 YVVF 71

RESULT 13

S00337
 legumin B LegK precursor - garden pea (fragment)
 N;Alternate names: minor legumin legk
 C;Species: Pisum sativum (garden pea)
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C;Accession: S00337; S02306
 R;Gatehouse, J.A.; Bown, D.; Gilroy, J.; Levasseur, M.; Castleton, J.; Ellis, T.H.N.
 Biochem. J. 250, 15-24, 1988
 A;Title: Two genes encoding 'minor' legumin polypeptides in pea (Pisum sativum L.).
 A;Reference number: S00336; MUID:88183306; PMID:3355508
 A;Accession: S00337
 A;Molecule type: DNA
 A;Residues: 1-350 <GAT>

A;Cross-references: UNIPROT:P05693; EMBL:X07015; MID:g20784; PIDN:CAA30068.1; PID:g20785
 A;Note: part of this sequence, including the amino end of the beta chain, was confirmed
 F;Domoney, C.; Barker, D.; Casey, R.
 Plant Mol. Biol. 7, 467-474, 1986
 A;Title: The complete deduced amino acid sequences of legumin beta-polypeptides from dif
 A;Reference number: S02306
 A;Accession: S02306
 A;Molecule type: mRNA
 A;Residues: 132-350 <DOM>
 A;Cross-references: EMBL:M16903
 A;Note: the nucleotide sequence contains a frameshift in codon 131
 F;1-169/Product: legumin B alpha chain #status experimental <ACH>
 C;Genetics:
 A;Gene: LegK
 A;Map position: 1
 A;Introns: 33/3; 225/3
 C;Superfamily: glycinin
 F;1-169/Product: legumin B beta chain #status experimental <ACH>
 F;170-350/Product: legumin B beta chain #status experimental <BCH>

Query Match 100.0%; Score 26; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVF 5
 |||||
 Db 291 YVVF 295

RESULT 14

T28978
 hypothetical protein T28A11.14 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T28978
 R;Rohlfing, T.
 submitted to the EMBL Data Library, January 1997
 A;Description: The sequence of C. elegans cosmid T28A11.

A;Reference number: Z20550
 A;Accession: T28978
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-373 <ROH>
 A;Cross-references: UNIPROT:P91509; EMBL:U80027; PIDN:AAC48124.1; GSPDB:GN00023; CESP:T28A11
 A;Experimental source: strain Bristol N2; clone T28A11
 C;Genetics:
 A;Gene: CESP:T28A11.14
 A;Map position: 5
 A;Introns: 52/3
 C;Superfamily: Caenorhabditis transposon Tc1 hypothetical 32K protein

Query Match 100.0%; Score 26; DB 2; Length 373;
 Best Local Similarity 100.0%; Pred. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVF 5
 |||||
 Db 347 YVVF 351

RESULT 15

AC0234
 Probable exported protein YP01919 [imported] - Yersinia pestis (strain CO92)
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 24-Nov-2003
 C;Accession: AC0234
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11586360
 A;Accession: AC0234
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-449 <KUR>
 A;Cross-references: GB:AL590842; PIDN:CAC90735.1; PID:g15979938; GSPDB:GN00175
 C;Genetics:
 A;Gene: YP01919
 C;Superfamily: uncharacterized conserved protein

Query Match 100.0%; Score 26; DB 2; Length 449;
 Best Local Similarity 100.0%; Pred. No. 11e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YVVF 5
 |||||
 Db 223 YVVF 227

Search completed: November 6, 2004, 19:54:11
 Job time : 15.1875 secs